

Figure 1A

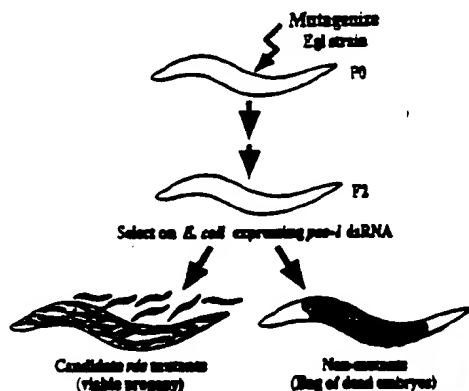


Figure B

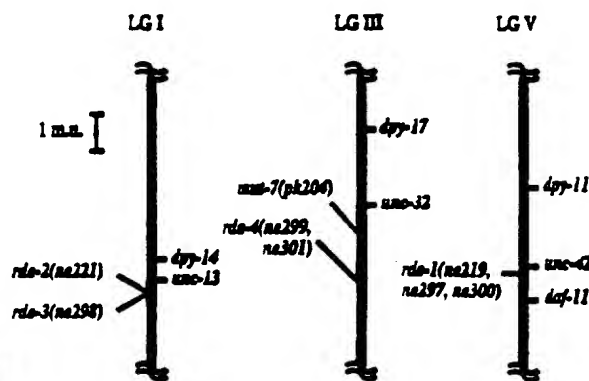


Figure 2

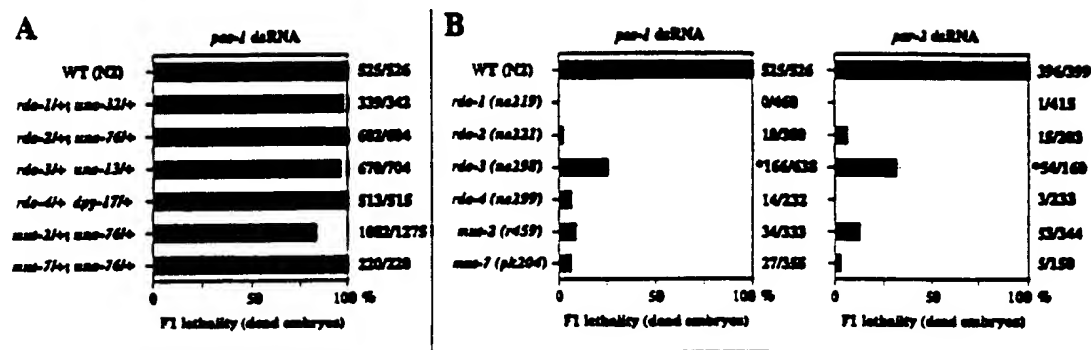


Figure 3

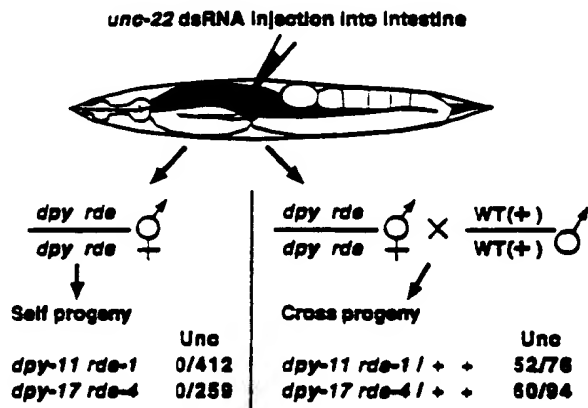
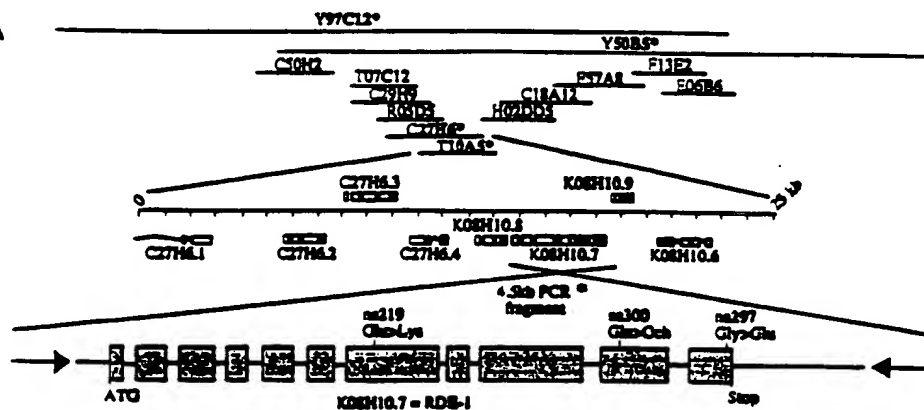


Figure 4

A



B

KDN-1	103	VS	.....
P48P7.1	118	.....	.....
o1P2C	77	.....	.....
SVLLS	116	.....	.....
SLing	120	.....	.....
KDN-1	167	.....	.....
P48P7.1	119	.....	.....
o1P2C	144	.....	.....
SVLLS	197	.....	.....
SLing	144	.....	.....
KDN-1	136	.....	.....
P48P7.1	489	.....	.....
o1P2C	220	.....	.....
SVLLS	172	.....	.....
SLing	168	.....	.....
KDN-1	424	.....	.....
P48P7.1	494	.....	.....
o1P2C	398	.....	.....
SVLLS	484	.....	.....
SLing	194	.....	.....
KDN-1	514	.....	.....
P48P7.1	501	.....	.....
o1P2C	192	.....	.....
SVLLS	543	.....	.....
SLing	483	.....	.....
KDN-1	604	.....	.....
P48P7.1	438	.....	.....
o1P2C	469	.....	.....
SVLLS	620	.....	.....
SLing	583	.....	.....
KDN-1	694	.....	.....
P48P7.1	728	.....	.....
o1P2C	538	.....	.....
SVLLS	691	.....	.....
SLing	621	.....	.....
KDN-1	790	.....	.....
P48P7.1	792	.....	.....
o1P2C	683	.....	.....
SVLLS	779	.....	.....
SLing	687	.....	.....
KDN-1	870	.....	.....
P48P7.1	868	.....	.....
o1P2C	870	.....	.....
SVLLS	893	.....	.....
SLing	766	.....	.....
KDN-1	960	.....	.....
P48P7.1	936	.....	.....
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SVLLS	931	.....	.....
SLing	827	.....	.....

SEQ ID NO: 3  
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09589992-101300

(SEQ ID NO: 1)

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17/1	ATG TCC TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG	31/11
Met ser ser asn phe pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu		
61/21	ATG AAA TGG CTT GCG AGG CCC ACT GGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA	91/31
met lys trp leu ala arg pro thr gly lys cys asp gly lys phe tyr glu lys lys val		
121/41	CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CCG GAA TAC TAC GAG	151/51
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu		
181/61	TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA	211/71
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys		
241/81	AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG	271/91
lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu		
301/101	AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT	331/111
lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr		
361/121	AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA	391/131
ser val cys arg leu asn thr val thr ser lys met leu val ser glu lys val val lys		
421/141	AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA	451/151
lys asp ser glu lys lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile		
481/161	CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA	511/171
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu		
541/181	GAA GCG AAT CGG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG	571/191
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala		
601/201	CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT	631/211
pro phe val asn glu glu ile lys val gln phe ala lys asn phe val tyr asp asn asn		
661/221	TCA ATT CTG CGA GTT CCT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA	691/231
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu		
721/241		751/251

STA GCA CCA ATC GAA GCA TGG TTT GGA ATT ATT GGA ATC AAA GAA TTG TTC GAT  
 val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp  
 731/261 811/271  
 GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG  
 gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met  
 841/281 871/291  
 TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA  
 ser leu leu asp tyr leu leu leu ile val asp pro gln ser cys asn asp asp val arg  
 901/301 931/311  
 AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA  
 lys asp leu lys thr lys leu met ala gly lys met thr ile arg gln ala ala arg pro  
 961/321 991/331  
 AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA  
 arg ile arg gln leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu  
 1021/341 1051/351  
 ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT  
 met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu  
 1081/361 1111/371  
 GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA  
 val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys tyr asp thr thr  
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 leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val  
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 AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG  
 lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu  
 1261/421 1291/431  
 AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA  
 lys pro gln arg tyr lys asn arg ile asp leu val met gln asp lys phe leu lys arg  
 1321/441 1351/451  
 GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT  
 ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp  
 1381/461 1411/471  
 TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG  
 phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gln met  
 1441/481 1471/491  
 ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA  
 ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gln  
 1501/501 1531/511  
 ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA  
 ile lys met thr pro val ile arg gly phe gln glu lys gln leu asn val val pro glu

AAA GAA GTT TGC TGT GGT GTT TTT GTA GTC AAC GAA ACA GCG GGA AAT CCA TGC TTA GAA  
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu

1851/351  
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA  
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile

CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT  
arg ile gly ala asn glu asn arg gly ala gln ser ile met tyr asp ala thr lys asn

GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC  
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala

GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG  
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gin lys val leu met

19917631  
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phe ile ile ile ser lys arg gin leu asn ala tyr gly phe val lys his tyr cys asp

19517851  
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA  
his thr ile gly val ala asn gln his ile thr ser glu thr val thr lys ala leu ala

2011/6/7  
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC  
ser leu arg his glu lys gly ser lys arg ile phe tyr gln ile ala leu lys ile asn

GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA  
ala lys leu gly gly ile asn gln glu leu asp trp ser glu ile ala glu ile ser pro

21517-21521

GPA GAA AAA GAA AGA CGG AAA ACA ATG CCA TTA ACT ATG TAT GTT CGA ATT GAT GTA ACT  
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr

21917731  
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT  
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn

CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG  
pro gly gly thr ile tyr arg asn met ile val thr gln glu glu cys arg pro gly glu

2511/771  
CGT GCA GTG GCT CAT GGA CGG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG  
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu

25717/91  
TTC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA  
Leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg



2401/801 2431/811  
 AAC GGA GTT AGC GAT TCG GAG ATG CTA CGT GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA  
 asp gly val ser asp ser glu met leu arg val ser his asp glu leu arg ser leu lys

2461/821 2491/831  
 AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG  
 ser glu val lys gln phe met ser glu arg asp gly glu asp pro glu pro lys tyr thr  
 2521/841 2551/851  
 TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG  
 phe ile val ile gln lys arg his asn thr arg leu leu arg arg met glu lys asp lys

2581/861 2611/871  
 CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA  
 pro val val asn lys asp leu thr pro ala glu thr asp val ala val ala val lys

2641/881 2671/891  
 CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA  
 gln trp glu glu asp met lys glu ser lys glu thr gly ile val asn pro ser ser gly

2701/901 2731/911  
 ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT  
 thr thr val asp lys leu ile val ser lys tyr lys phe asp phe phe leu ala ser his

2761/921 2791/931  
 CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA  
 his gly val leu gly thr ser arg pro gly his tyr thr val met tyr asp asp lys gly

2821/941 2851/951  
 ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT  
 met ser gln asp glu val tyr lys met thr tyr gly leu ala phe leu ser ala arg cys

2881/961 2911/971  
 CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG  
 arg lys pro ile ser leu pro val pro val his tyr ala his leu ser cys glu lys ala

2941/981 2971/991  
 AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT  
 lys glu leu tyr arg thr tyr lys glu his tyr ile gly asp tyr ala gln pro arg thr

3001/1001 3031/1011  
 CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA  
 arg his glu met glu his phe leu gln thr asn val lys tyr pro gly met ser phe ala

3061/1021 3091/1031  
 TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT  
 OCH (SEQ ID NO: 3)

3121/1041 3151/1051  
 TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3181/1061  
 CTT GAA ATT TAA AAA AAA AAA AAA AAA (SEQ ID NO: 2)

Figure 7

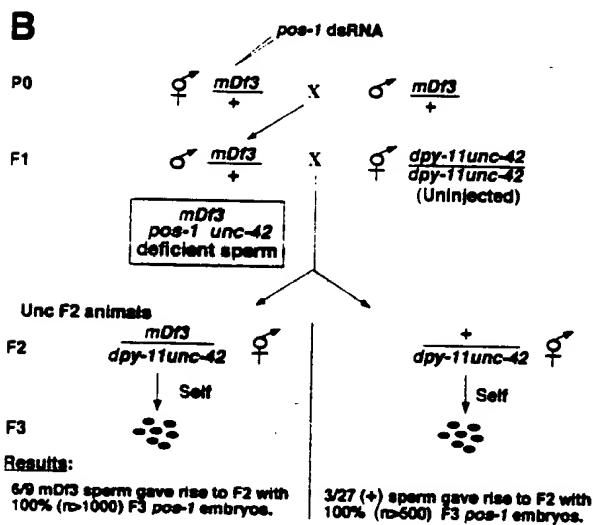
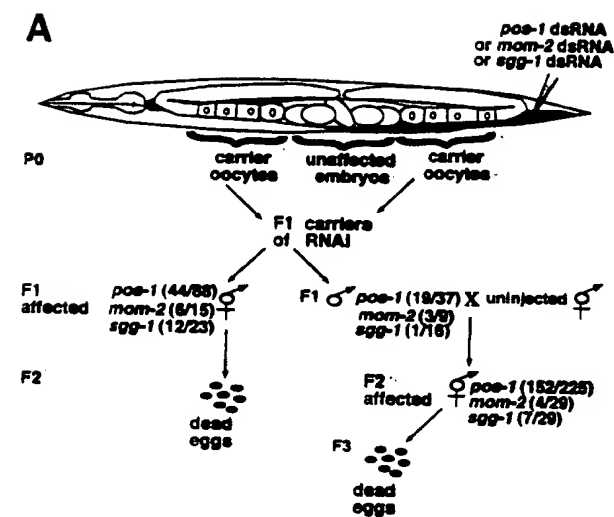


Figure 8

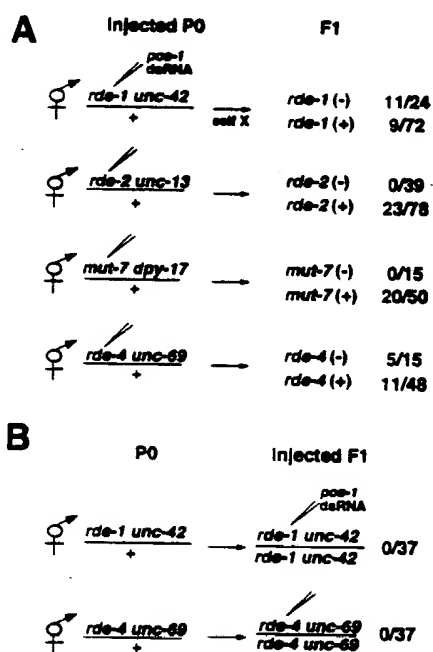
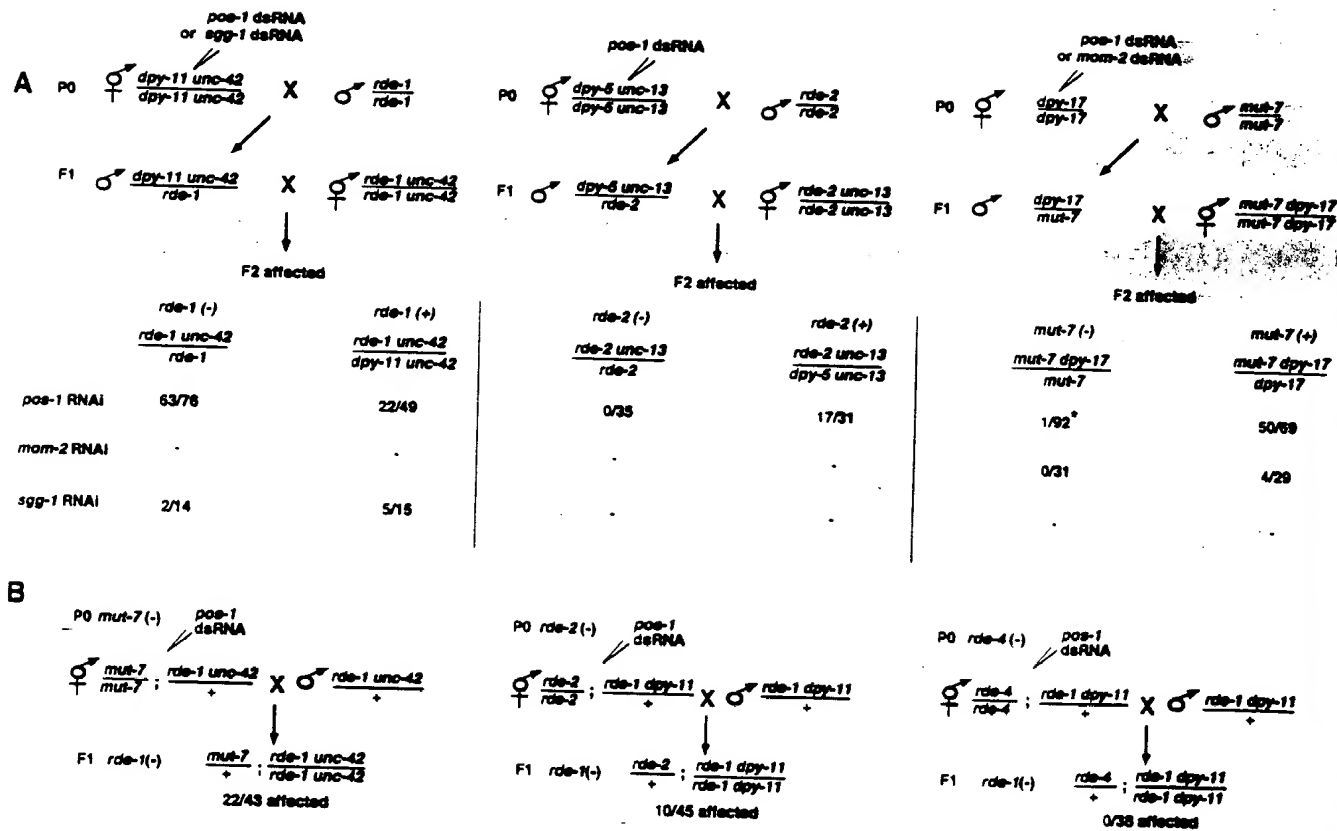


Figure 9



100-443886-1

10 20 30 40 50 60  
ATGGATTTAACCAAACCTGTTTGAAGCGTTTTCGGTGGATCAGATGTTCTCTATGAAG  
M D L T K L T F E S V F G G S D V P M K

70 80 90 100 110 120  
CCTTCCCGATCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTGAGATGTTTCTG  
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180  
AAGAAAACCTCCCTCATGGTACTAGAAGAGGCTGCTAAGGCTGTCTATCAAAGACGCCA  
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240  
ACTTGGGGCACTGTGGAACCTTCTGAAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT  
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300  
ACTGTAAAAGGCCAGGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT  
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360  
TTACGCAAGGTTGTGGAGAAAGGAAAGCACGAAATCTTTTTCATTCTCTGGAACAACCAA  
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420  
GAAGAAGCTCTTTTGAATATTGATCAAATATCGGATAAGGCTGAGGAATTGAAACGATCA  
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480  
ACTTCAGATGCTGTTTCAAGGATAACGATAACGATGATTTCGATTCTCTACAAGTCTGAATTT  
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540  
CCACCTGGTATTTGCGCAACCGAGAATTGGGTGCGGAAAGTTGCAGGAAAAATCTCAAAA  
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600  
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGATGAGAGAACCGAGCGTTTCTTG  
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660  
GTTATATGCACGATGTGCAATCAAAAAACCAGAGGAATCAGAAGTAAGAAGAAGGACGCA  
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720  
AAGAATCTTGCAGCATGGTTGATGTGGAAAGCGTTGGAAGACGGTATCGAATCTCTGGAA  
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780  
TCATATGATATGGTTGATGTGATTGAAAATTTGGAAGAAGCTGAACATTTACTCGAAATT  
S Y D M V D V I E N L E E A E H L L E I

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**TTATAAAAAAAAAAAAAAAAAA** (SEQ ID NO:4)  
L \* K K K K K (SEQ ID NO:5)

00E70T" 2656395d

Figure 11

